

1

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD.,

<120> NOVEL POLYPEPTIDE

<130> 11152W01

<150> JP H10-241248

<151> 1998-08-27

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 475

<212> PRT

<213> Homo sapiens

<400> 1

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Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

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Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp
 35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser
 50 55 60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe
 65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly
 85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr
 100 105 110

Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg
 115 120 125

Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala
 130 135 140

Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp
 145 150 155 160

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser
 165 170 175

Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser
 180 185 190

Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly
 195 200 205

Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser
 210 215 220

Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 225 230 235 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr
 245 250 255

Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly
 260 265 270

Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser
 275 280 285

Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys
 290 295 300

Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser
 305 310 315 320

Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly
325 330 335

Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe
340 345 350

Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp
355 360 365

Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu
370 375 380

Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro
385 390 395 400

Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
405 410 415

Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
420 425 430

Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
435 440 445

Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly
450 455 460

Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile

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<210> 2

<211> 2240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)..(1451)

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Met Ala Val Val Ser Glu Asp Asp Phe Gln

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His Ser Ser Asn Ser Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala

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gac cag gag gca ctg ctt gag aag ctg ctg gac cgc ccg ccc cct ggc 149

Asp Gln Glu Ala Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly

30

35

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ctg cag agg ccc gag gac cgc ttc tgt ggc aca tac atc atc ttc ttc	197
Leu Gln Arg Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe	
45 50 55	
agc ctg ggc att ggc agt cta ctg cca tgg aac ttc ttt atc act gcc	245
Ser Leu Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala	
60 65 70	
aag gag tac tgg atg ttc aaa ctc cgc aac tcc tcc agc cca gcc acc	293
Lys Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr	
75 80 85 90	
ggg gag gac cct gag ggc tca gac atc ctg aac tac ttt gag agc tac	341
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr	
95 100 105	
ctt gcc gtt gcc tcc acc gtg ccc tcc atg ctg tgc ctg gtg gcc aac	389
Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val Ala Asn	
110 115 120	
ttc ctg ctt gtc aac agg gtt gca gtc cac atc cgt gtc ctg gcc tca	437
Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val Leu Ala Ser	
125 130 135	
ctg acg gtc atc ctg gcc atc ttc atg gtg ata act gca ctg gtg aag	485
Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr Ala Leu Val Lys	
140 145 150	

gtg gac act ttc tcc tgg acc cgt ggc ttt ttt gcg gtc acc att gtc 533
 Val Asp Thr Phe Ser Trp Thr Arg Gly Phe Phe Ala Val Thr Ile Val
 155 160 165 170

tgc atg gtg atc ctc agc ggt gcc tcc act gtc ttc agc agc agc atc 581
 Cys Met Val Ile Leu Ser Gly Ala Ser Thr Val Phe Ser Ser Ser Ile
 175 180 185

tac ggc atg acc ggc tcc ttt cct atg agg aac tcc cag gca ctg ata 629
 Tyr Gly Met Thr Gly Ser Phe Pro Met Arg Asn Ser Gln Ala Leu Ile
 190 195 200

tca gga gga gcc atg ggc ggg acg gtc agc gcc gtg gcc tca ttg gtg 677
 Ser Gly Gly Ala Met Gly Gly Thr Val Ser Ala Val Ala Ser Leu Val
 205 210 215

gac ttg gct gca tcc agt gat gtg agg aac agc gcc ctg gcc ttc ttc 725
 Asp Leu Ala Ala Ser Ser Asp Val Arg Asn Ser Ala Leu Ala Phe Phe
 220 225 230

ctg acg gcc acc atc ttc ctc gtg ctc tgc atg gga ctc tac ctg ctg 773
 Leu Thr Ala Thr Ile Phe Leu Val Leu Cys Met Gly Leu Tyr Leu Leu
 235 240 245 250

ctg tcc agg ctg gag tat gcc agg tac tac atg agg cct gtt ctt gcg 821
 Leu Ser Arg Leu Glu Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala

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gcc cat gtg ttt tct ggt gaa gag gag ctt ccc cag gac tcc ctc agt 869

Ala His Val Phe Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser

270

275

280

gcc cct tcg gtg gcc tcc aga ttc att gat tcc cac aca ccc cct ctc 917

Ala Pro Ser Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu

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cgc ccc atc ctg aag aag acg gcc agc ctg ggc ttc tgt gtc acc tac 965

Arg Pro Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr

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gtc ttc ttc atc acc agc ctc atc tac ccc gcc gtc tgc acc aac atc 1013

Val Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile

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gag tcc ctc aac aag ggc tcg ggc tca ctg tgg acc acc aag ttt ttc 1061

Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe

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atc ccc ctc act acc ttc ctc ctg tac aac ttt gct gac cta tgt ggc 1109

Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly

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cgg cag ctc acc gcc tgg atc cag gtg cca ggg ccc aat agc aag gcg 1157

9.

Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn Ser Lys Ala

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ctc cca ggg ttc gtg ctc ctc cgg acc tgc ctc atc ccc ctc ttc gtg 1205

Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile Pro Leu Phe Val

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390

ctc tgt aac tac cag ccc cgc gtc cac ctg aag act gtg gtc ttc cag 1253

Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys Thr Val Val Phe Gln

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tcc gat gtg tac ccc gca ctc ctc agc tcc ctg ctg ggg ctc agc aac 1301

Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn

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ggc tac ctc agc acc ctg gcc ctc ctc tac ggg cct aag att gtg ccc 1349

Gly Tyr Leu Ser Thr Leu Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro

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agg gag ctg gct gag gcc acg gga gtg gtg atg tcc ttt tat gtg tgc 1397

Arg Glu Leu Ala Glu Ala Thr Gly Val Val Met Ser Phe Tyr Val Cys

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455

ttg ggc tta aca ctg ggc tca gcc tgc tct acc ctc ctg gtg cac ctc 1445

Leu Gly Leu Thr Leu Gly Ser Ala Cys Ser Thr Leu Leu Val His Leu

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atc tag aagggaggac acaaggacat tgggtgcttca gagcctttga agatgagaag 1501

Ile

475

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agcagagcac actcgggcct caicccctccc aagatgccag tgagccacgt ccatgcccac 1621

tccgtgcaag gcagatatc cagtcatatt aacagaacac tcctgagaca gttgaagaag 1681

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tagcccttca aagatgctgc cagtgttcgc cctagagtta ttacaaagcc agtgccaaaa 1801

cccagccatg ggctctttgc aacctcccag ctgcgctcat tccagctgac agcgagatgc 1861

aagcaaatgc tcagctctcc ttaccttgaa ggggtctccc tggaatggaa gtcccctggc 1921

atggtcagtc ctcaggccca agactcaagt gtgcacagac ccctgtgttc tgtgggtgaa 1981

caactgcca ctaaccagac tggaaaaccc agaaagatgg gccttccatg aatgcttcat 2041

tccagaggga ccagagggcc tccctgtgca agggatcaag catgtctggc ctgggttttc 2101

aaaaaaagag ggatcctcat gacctggtgg tctatggcct gggtaagat gagggctttt 2161

cagtgttcct gttacaaca tgcataagcc attggttcaa gggcgtaata aatactigcg 2221

tattcaaaaa aaaaaaaaaa

2240

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 5

<211> 475

<212> PRT

<213> Rat

<400> 5

Met Ala Phe Ala Ser Glu Asp Ile Ala Tyr His Ser Ser Asn Ala Val
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Tyr Arg Val Pro Ser Asn Arg His Glu Ala Asp Gln Glu Ala Leu Leu
 20 25 30

Gly Lys Pro Leu Asp Tyr Pro Ala Pro Gly Leu Gln Arg Pro Glu Asp
 35 40 45

Arg Phe Asn Gly Ala Tyr Ile Ile Phe Phe Cys Leu Gly Ile Gly Gly
 50 55 60

Leu Leu Pro Trp Asn Phe Phe Val Thr Ala Lys Glu Tyr Trp Ala Phe
 65 70 75 80

Lys Leu Arg Asn Cys Ser Ser Pro Ala Ser Gly Lys Asp Pro Glu Asp
 85 90 95

Ala Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr
 100 105 110

Val Pro Ser Leu Leu Phe Leu Val Ala Asn Phe Leu Leu Val Asn Arg
 115 120 125

Ile Arg Val His Val Arg Val Leu Ala Ser Leu Ser Val Ser Leu Ala
 130 135 140

13.

Ile Phe Val Val Met Ala Val Leu Val Arg Val Asp Thr Ser Ser Trp
145 150 155 160

Thr Arg Gly Phe Phe Ser Ile Ala Met Ala Cys Met Ala Ile Ile Ser
 165 170 175

Ser Ser Ser Thr Ile Phe Asn Ser Ser Val Tyr Gly Leu Thr Gly Ser
 180 185 190

Phe Pro Met Arg Asn Ala Gln Ala Leu Ile Ser Gly Gly Ala Met Gly
 195 200 205

Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser
 210 215 220

Asp Val Arg Asp Ser Ala Leu Ala Phe Phe Leu Thr Ala Ala Val Phe
225 230 235 240

Leu Gly Leu Cys Val Gly Leu Tyr Leu Leu Leu Pro Gln Leu Glu Tyr
 245 250 255

Ala Arg Tyr Tyr Met Arg Pro Val Val Pro Ile His Val Phe Ser Ser
 260 265 270

Glu Asp Ser Pro Pro Arg Asp Ala Pro Ser Thr Ser Ser Val Ala Pro
 275 280 285

Ala Ser Arg Ala Val His Thr Pro Pro Leu Gly Pro Ile Leu Lys Lys
 290 295 300

Thr Ala Gly Leu Gly Phe Cys Ala Val Phe Leu Tyr Phe Ile Thr Ala
305 310 315 320

14.

Leu Ile Phe Pro Ala Ile Ser Thr Asn Ile Gln Pro Met His Lys Gly
325 330 335

Thr Gly Ser Pro Trp Thr Ser Lys Phe Tyr Val Pro Leu Thr Val Phe
340 345 350

Leu Leu Phe Asn Phe Ala Asp Leu Cys Gly Arg Gln Val Thr Ala Trp
355 360 365

Ile Gln Val Pro Gly Pro Arg Ser Lys Leu Leu Pro Ile Leu Ala Val
370 375 380

Ser Arg Val Cys Leu Val Pro Leu Phe Leu Leu Cys Asn Tyr Gln Pro
385 390 395 400

Arg Ser His Leu Thr Leu Val Leu Phe Gln Ser Asp Ile Tyr Pro Ile
405 410 415

Leu Phe Thr Cys Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
420 425 430

Val Leu Met Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
435 440 445

Thr Ser Val Val Met Leu Phe Tyr Met Ser Leu Gly Leu Met Leu Gly
450 455 460

Ser Ala Cys Ala Ala Leu Leu Glu His Phe Ile
465 470 475

<210> 6

<211> 1734

<212> DNA

<213> Rat

<220>

<221> CDS

<222> (12)..(1436)

<223> Description of Artificial Sequence: synthetic DNA

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Asn Ala Val Tyr Arg Val Pro Ser Asn Arg His Glu Ala Asp Gln Glu	
15 20 25	
gcc cta ctg gga aaa cca cta gac tac cca gcc cca ggc ctg cag agg	146
Ala Leu Leu Gly Lys Pro Leu Asp Tyr Pro Ala Pro Gly Leu Gln Arg	
30 35 40 45	
cca gag gac cgc ttc aat ggt gcc tat atc atc ttc ttc tgc ctg gga	194
Pro Glu Asp Arg Phe Asn Gly Ala Tyr Ile Ile Phe Phe Cys Leu Gly	
50 55 60	
att ggc ggc cta cta ccc tgg aac ttt ttt gtc act gcc aaa gag tac	242
Ile Gly Gly Leu Leu Pro Trp Asn Phe Phe Val Thr Ala Lys Glu Tyr	
65 70 75	
igg gca ttt aaa ctc cga aac tgc tcc agc cca gcc tcc ggg aag gac	290
Trp Ala Phe Lys Leu Arg Asn Cys Ser Ser Pro Ala Ser Gly Lys Asp	

80

85

90

cca gag gat gca gac atc ctg aac tac ttt gag agc tac ctg gcg gtt 338
 Pro Glu Asp Ala Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val
 95 100 105

gct tcc act gtg cct tcc ctg ctg ttt ctg gtg gct aac ttc ctg ctt 386
 Ala Ser Thr Val Pro Ser Leu Leu Phe Leu Val Ala Asn Phe Leu Leu
 110 115 120 125

gtc aac agg atc cgg gtg cat gtc cga gtt ctg gcc tca ctg tcc gtc 434
 Val Asn Arg Ile Arg Val His Val Arg Val Leu Ala Ser Leu Ser Val
 130 135 140

tcc ctg gcc atc ttt gtg gtt atg gcc gtg ctg gtg agg gtg gac act 482
 Ser Leu Ala Ile Phe Val Val Met Ala Val Leu Val Arg Val Asp Thr
 145 150 155

tct tcc tgg acc cgg ggc ttc ttc agc atc gcc atg gcg tgc atg gcc 530
 Ser Ser Trp Thr Arg Gly Phe Phe Ser Ile Ala Met Ala Cys Met Ala
 160 165 170

atc atc agc agc tcc tcc acc atc ttc aat agc agc gtg tat ggc ctg 578
 Ile Ile Ser Ser Ser Ser Thr Ile Phe Asn Ser Ser Val Tyr Gly Leu
 175 180 185

acg ggc tcg ttc ccc atg agg aat gcc cag gca ctg ata tca gga gga 626
 Thr Gly Ser Phe Pro Met Arg Asn Ala Gln Ala Leu Ile Ser Gly Gly
 190 195 200 205

gcc atg gga ggg aca gtc agc gcc gtg gcc tcc ctg gtg gac ctg gca 674
 Ala Met Gly Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala
 210 215 220

gca tcc agt gac gtg cga gac agt gcg ctg gcc ttc ttc ctc aca gca 722
 Ala Ser Ser Asp Val Arg Asp Ser Ala Leu Ala Phe Phe Leu Thr Ala
 225 230 235

17.

gca gtc ttc ctt ggg ctc tgt gtg ggg ctc tac cta ctg ctg ccc caa	770
Ala Val Phe Leu Gly Leu Cys Val Gly Leu Tyr Leu Leu Leu Pro Gln	
240 245 250	
ctg gag tat gcc agg tac tac atg agg ccg gtt gtc cca atc cac gtg	818
Leu Glu Tyr Ala Arg Tyr Tyr Met Arg Pro Val Val Pro Ile His Val	
255 260 265	
ttt tct agt gaa gac agc cca ccc cgg gat gct ccc agc acc tcc tcc	866
Phe Ser Ser Glu Asp Ser Pro Pro Arg Asp Ala Pro Ser Thr Ser Ser	
270 275 280 285	
gtg gcc cct gca tcc aga gca gtg cac acg cca ccc ctc gga ccc atc	914
Val Ala Pro Ala Ser Arg Ala Val His Thr Pro Pro Leu Gly Pro Ile	
290 295 300	
ctg aag aag aca gct ggc ctg ggg ttc tgc gcc gtt ttc ctc tac ttc	962
Leu Lys Lys Thr Ala Gly Leu Gly Phe Cys Ala Val Phe Leu Tyr Phe	
305 310 315	
atc acc gcc ctt atc ttc ccc gct atc tcc acc aac atc cag ccc atg	1010
Ile Thr Ala Leu Ile Phe Pro Ala Ile Ser Thr Asn Ile Gln Pro Met	
320 325 330	
cac aag ggc acc ggc tct cca tgg acc tcc aag ttc tat gtg ccc ctc	1058
His Lys Gly Thr Gly Ser Pro Trp Thr Ser Lys Phe Tyr Val Pro Leu	
335 340 345	
acc gtc ttc ctc ctt ttc aac ttt gct gac ctc tgc ggc cga cag gtc	1106
Thr Val Phe Leu Leu Phe Asn Phe Ala Asp Leu Cys Gly Arg Gln Val	
350 355 360 365	
aca gcc tgg atc cag gtg cca ggt cct agg agc aag ctg ctc ccc ata	1154
Thr Ala Trp Ile Gln Val Pro Gly Pro Arg Ser Lys Leu Leu Pro Ile	
370 375 380	
ctg gca gtc tct cgc gtc tgc ctc gtg cct ctc ttc ctg ctc tgt aac	1202
Leu Ala Val Ser Arg Val Cys Leu Val Pro Leu Phe Leu Leu Cys Asn	

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390

395

tac cag cca cgc tca cac ctg act ctg gtg ctt ttc cag tct gac atc 1250
 Tyr Gln Pro Arg Ser His Leu Thr Leu Val Leu Phe Gln Ser Asp Ile
 400 405 410

tac cct ata ctc ttc acc tgc ctc ttg ggg ctc agt aat ggc tac ctc 1298
 Tyr Pro Ile Leu Phe Thr Cys Leu Leu Gly Leu Ser Asn Gly Tyr Leu
 415 420 425

agc acg ctg gtg ctc atg tat ggg ccc aag att gtg ccc cgg gag ctg 1346
 Ser Thr Leu Val Leu Met Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu
 430 435 440 445

gct gag gcc acc agt gtg gtg atg ctg ttc tac atg tca ctg ggt ttg 1394
 Ala Glu Ala Thr Ser Val Val Met Leu Phe Tyr Met Ser Leu Gly Leu
 450 455 460

atg ctg ggc tca gcc tgt gcg gcc ttg ctt gag cac ttt atc taggagggg 1445
 Met Leu Gly Ser Ala Cys Ala Ala Leu Leu Glu His Phe Ile
 465 470 475

cggcaaggat gtgggttctg tgtgagttag ttgtggtttgg gtccctggga cctggacagg 1505
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 gccactcag actgtctttc tctcagacac atccttgac atcttgttca aggagacatt 1625
 ccagacacag cccagcatgg tggctcacac ctgtaatccc agcattcaag aggctggagc 1685
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<210> 7

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 7

arrtancrct tact

14

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 8

ytnccntgga acttttt

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